

SEQUENCE LISTING

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 34 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

GACTCGCTGC AGATCGATT TTTTTTTTTT TTTT

34

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 30 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GCCATCAAGC CACCCAAGAA CTCTTAAC TT

30

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 30 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

CCAATAGCCA GACCATTATA TACACTAATT

30

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 310 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

GCTTATAGAA GGACCCCTAG TATGGGGTAA TCCCCTCTGG GAAACCAAGC CCCACTACTC	60
AGCAGGAAAA ATAGAATAGG AAACCTCACCA AGGACATACT TTCCCTCCCT CCAGATGGCT	120
AGCCACTGAG GAAGGAAAAA TACTTCACC TGCACTAAC CACAGAAAT TACTTAAAAC	180
CCTTCACCAA ACCTTCCACT TAGGCATTGA TAGCACCCAT CAGATGGCCA AATTATTATT	240
TACTGGACCA GGCCTTTCA AACTATCAA GAAGATAGTC AGGGGCTGTG AAGTGTGCCA	300
AAGAAATAAT	310

(2) INFORMATION FOR SEQ ID NO: 113:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Leu Ile Glu Gly Pro Leu Val Trp Gly Asn Pro Leu Trp Glu Thr Lys

1 5 10 15

Pro Gln Tyr Ser Ala Gly Lys Ile Glu Xaa Glu Thr Ser Gln Gly His

20 25 30

Thr Phe Leu Pro Ser Arg Trp Leu Ala Thr Glu Glu Gly Lys Ile Leu

35 40 45

Ser Pro Ala Ala Asn Gln Gln Lys Leu Leu Lys Thr Leu His Gln Thr

50 55 60

Phe His Leu Gly Ile Asp Ser Thr His Gln Met Ala Lys Leu Leu Phe

65 70 75 80

Thr Gly Pro Gly Leu Phe Lys Thr Ile Lys Lys Ile Val Arg Gly Cys

85 90 95

Glu Val Cys Gln Arg Asn Asn

100

(2) INFORMATION FOR SEQ ID NO: 114:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 635 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

CCCTGTATCT TTAACCTCCT TGTAAAGTTT GTCTCTTCCA GAATCAAAAC TGTAAAAC 60
CAAATTGTTTC TTCAAATGGA GCACCCAGATG GAGTCCATGA CTAAGATCCA CCGTGGACCC 120
CTGGACCGGC CTGCTAGCCC ATGCTCCGAT GTTAATGACA TTGAAGGCAC CCCTCCCGAG 180
GAAATCTCAA CTGCACAACC CCTACTATGC CCCAATTCA CGGGAAAGCAC TTAGACCGGT 240
CATCAGCCAA CCTCCCCAAC ACCACTTGGG TTTTCTCTT GAGAGGGGGG ACTGAGAGAC 300
AGGACTAGCT GGATTTCCTA GGCCAAACGAA GAATCCCTAA CCCTAGCTGG CAAGGTGACT 360
GCATCCACCT CTAAACATGG GCCTTGCAAC TTAGCTCACA CCCGACCAAT CAGAGAGCTC 420
ACTAAAATGC TAATTAGGCA AAAATAGGAG GTAAAGAAAT AGCCAATCAT CTATTGCCCTG 480
AGAGCACAGC GGGAGGGACA AGGATCGGGGATAAAACCA GGCAATTGGAG CCGGCAACGG 540
CAACCCCCCTT TGGGTCCCCCT CCCTTTGTAT GGGCGCTCTG TTTTCACTCT ATTTCACCT 600
ATTAATCTT GCAACTGAAA AAAAAAAA AAAAA 635

(2) INFORMATION FOR SEQ ID NO: 115

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

5

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

Pro Cys Ile Phe Asn Leu Leu Val Lys Phe Val Ser Ser Arg Ile Lys

1 5 10 15

Thr Val Lys Leu Gln Ile Val Leu Gln Met Glu His Gln Met Glu Ser

20 25 30

Met Thr Lys Ile His Arg Gly Pro Leu Asp Arg Pro Ala Ser Pro Cys

35 40 45

Ser Asp Val Asn Asp Ile Glu Gly Thr Pro Pro Glu Glu Ile Ser Thr

50 55 60

Ala Gln Pro Leu Leu Cys Pro Asn Ser Ala Gly Ser Ser

10

65 70 75

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleotide
- 5 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

TGGGGTTCCA TTTGTAAGAC CATCTGTAGC TT

32

10

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1481 base pairs
- (B) TYPE: nucleotide
- 15 (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

ATGGCCCTCC CTTATCATAc TTTTCTCTTT ACTGTCTCT TACCCCTTT CGCTCTCACT 60
GCACCCCCTC CAGCTGCTG TACAACCAGT AGCTCCCCTT ACCAAGAGTT TCTATGAACA 120
ACGGGGCTTC CTGGAAATAT TGATGCCCA TCATATAGGA GTTTATCTAA GGGAAACTCC 180
ACCTTCACTG CCCACACCCA TATGCCCGC AACTGCTATA ACTCTCCAC TCTTTGCATG 240
CATGCAAATA CTCATTATTG GACAGGGAAA ATGATTATTC CTAGTTGTCC TGGAGGACTT 300
GGAGCCACTG TCTGTTGGAC TTACTTCACC CATAACAGTA TGTCTGATGG GGGTGGAAATT 360
CAAGGTCAGG CAAGAGAAAA ACAACTAAGG GAAGGAAATCT CCCAACTGAC CCGGGGGACAT 420
AGCACCCCTA GCCCCAACAA AGGACTAGTT CTCTCAAAAC TACATGAAAC CCTCCGTACC 480
CATACTCGCC TGGTGAGCCT ATTTAATACC ACCCTCACTC GGCTCCATGA GGTCTCAGCC 540
CAAAACCTA CTAACGTG TGATGTGCCTC CCCCCTGCACT TCAGGGCATA CATTCAATC 600
CCTGTTCTG AACAAATGGAA CAACTTCAGC ACAGAAATAA ACACCACTTC CGTTTTAGTA 660
GGACCTCTTG TTTCCAATCT GGAAATAACC CATAACCTCAA ACCTCACCTG TGAAAATTT 720
AGCAATACTA TAGACACAAAC CAGCTCGGAA TGCACTAGGT GGGTAACACC TCCCACACGA 780
ATAGTCTGCC TACCCCTCAGG AATAATTTT GTCTGTTGGTA CCTCAGCCTA TCATTGTTG 840
AATGGCTCTT CAGAACTAT GTGCTCTCTC TCATTCTTAG TGCCCCCTAT GACCATCTAC 900
ACTGAACAAG ATTATACAA TCATGTGCTA CCTAAGCCCC ACAACRAAAG AGTACCCATT 960
CTTCCTTTTG TTATCAGAGC AGGAGTGCTA GCCAGACTAG CTACTGGCAT TGGCAGTATC 1020

20

ACAAACCTCTA CTCAGTTCTA CTACAAACTA TCTCAAGAAA TAAATGGTGA CATCGAACAG 1080
GTCACTGACT CCCTGGTCAC CTTGCAAGAT CAACTTAAC CCCTAGCAGC AGTAGTCCTT 1140
CAAAATCGAA GAGCTTTAGA CTTGCTAACCC GCCAAAAGAG GGGGAACCTG TTTATTTTTA 1200
GGAGAAGAAC GCTGTTATTA TGTTAATCAA TCCAGAATTG TCACTGAGAA AGTTAAAGAA 1260
ATTCGAGATC GAATACAATG TAGAGCAGAG GAGCTCAAA ACACCGAACG CTGGGGCCTC 1320
CTCAGCCAAT GGATGCCCTG GGTTCTCCCC TTCTTAGGAC CTCTAGCAGC TCTAATATTG 1380
TTACTCCTCT TTGGACCCTG TATCTTTAAC CTCCTGTAA AGTTGTCTC TTCCAGAATT 1440
GAAGCTGTAA AGCTACAGAT GGTCTTACAA ATGGAACCCC A 1481

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 493 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

Met Ala Leu Pro Tyr His Thr Phe Leu Phe Thr Val Leu Leu Pro Pro
1 5 10 15
Phe Ala Leu Thr Ala Pro Pro Pro Cys Cys Cys Thr Thr Ser Ser Ser
20 25 30
Pro Tyr Gln Glu Phe Leu Xaa Arg Thr Arg Leu Pro Gly Asn Ile Asp
35 40 45
Ala Pro Ser Tyr Arg Ser Leu Ser Lys Gly Asn Ser Thr Phe Thr Ala
50 55 60
His Thr His Met Pro Arg Asn Cys Tyr Asn Ser Ala Thr Leu Cys Met
65 70 75 80
His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys
85 90 95
Pro Gly Gly Leu Gly Ala Thr Val Cys Trp Thr Tyr Phe Thr His Thr
100 105 110
Ser Met Ser Asp Gly Gly Gly Ile Gln Gly Gln Ala Arg Glu Lys Gln
115 120 125
Val Lys Glu Ala Ile Ser Gln Leu Thr Arg Gly His Ser Thr Pro Ser
130 135 140
Pro Tyr Lys Gly Leu Val Leu Ser Lys Leu His Glu Thr Leu Arg Thr

145 150 155 160
His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Arg Leu His
165 170 175
Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Met Cys Leu Pro Leu
180 185 190
His Phe Arg Pro Tyr Ile Ser Ile Pro Val Pro Glu Gln Trp Asn Asn
195 200 205
Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Val
210 215 220
Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe
225 230 235 240
Ser Asn Thr Ile Asp Thr Thr Ser Ser Gln Cys Ile Arg Trp Val Thr
245 250 255
Pro Pro Thr Arg Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys
260 265 270
Gly Thr Ser Ala Tyr His Cys Leu Asn Gly Ser Ser Glu Ser Met Cys
275 280 285
Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp
290 295 300
Leu Tyr Asn His Val Val Pro Lys Pro His Asn Lys Arg Val Pro Ile
305 310 315 320
Leu Pro Phe Val Ile Arg Ala Gly Val Leu Gly Arg Leu Gly Thr Gly
325 330 335
Ile Gly Ser Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln
340 345 350
Glu Ile Asn Gly Asp Met Glu Gln Val Thr Asp Ser Leu Val Thr Leu
355 360 365
Gln Asp Gln Leu Asn Ser Leu Ala Ala Val Val Leu Gln Asn Arg Arg
370 375 380
Ala Leu Asp Leu Leu Thr Ala Lys Arg Gly Gly Thr Cys Leu Phe Leu
385 390 395 400
Gly Glu Glu Arg Cys Tyr Tyr Val Asn Gln Ser Arg Ile Val Thr Glu
405 410 415
Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Cys Arg Ala Glu Glu Leu
420 425 430
Gln Asn Thr Glu Arg Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Val

435

440

445

Leu Pro Phe Leu Gly Pro Leu Ala Ala Leu Ile Leu Leu Leu Leu Phe

450

455

460

Gly Pro Cys Ile Phe Asn Leu Leu Val Lys Phe Val Ser Ser Arg Ile

465

470

475

480

Glu Ala Val Lys Leu Gln Met Val Leu Gln Met Glu Pro

485

490

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

TCAAAATCGA AGAGCTTTAG ACTTGCTAAC CG

32

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 1329 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

TCAAAATCGA AGAGCTTTAG ACTTGCTAAC CCCCAAAAAGA GGGGGAAACCT GTTTATTTT 60
AGGGGAAGAA TGCTGTTAGT ATCTTAATCA ATCTGGAATC ATTACTGAGA AAGTTAAAGA 120
AATTGAGAT CGAATATAAT GTAGAGCAGA GGACCTTCAA AACACTGCAC CCTGGGGCCT 180
CCTCAGCCAA TGGATGCCCT GGACTCTCCC CTTCTTAGGA CCTCTAGCAG CTATAATATT 240
TTTACTCCCT TTGGACCCCT GTATCTCAA CTTCTTGT 300
TGAAGCTGTA AAGCTACAAA TAGTTCTCA AATGGAACCC CAGATGCCAGT CCATGACTAA 360
AATCTACCGT GGACCCCTGG ACCGGCCTGC TAGACTATGC TCTGATGTTA ATGACATTGA 420
AGTCACCCCT CCCGAGGAAA TCTCAACTGC ACAACCCCTA CTACACTCCA ATTCACTAGG 480
AAGCAGTTAG AGCAGTTGTC AGCCAACCTC CCCAACAGTA CTTGGTTTT CCTGTTGAGA 540
GGGTGGACTG AGAGACAGGA CTAGCTGGAT TTCCTAGGCT GACTAAGAAT CCCNAAGCCT 600

ANCTGGGAAG GTGACCCAT CCATCTTAA ACATGGGCT TGCAACTTAG CTCACACCCG 660
ACCAATCAGA GAGCTCACTA AAATGCTAAT CAGGCAAAAA CAGGAGGTAACCAATAGCC 720
AATCATCTAT TGCCTGAGAG CACAGCGGGA AGGACAAGGA TTGGGATATA AACTCAGGCC 780
TTCAAGCCAG CAACAGCAAC CCCCTTGGA TCCCCTCCA TTGTATGGGA GCTCTGTTT 840
CACTCTATTCT CACTCTATTA AATCATGCAA CTGCACCTT CTGGTCCGTG TTTTTATGG 900
CTCAAGCTGA GCTTTTGTTC GCCATCCACC ACTGCTGTT GCCACCGTCA CAGACCCGCT 960
GCTGACTTCC ATCCCTTGGA ATCCAGCAGA GTGTCCACTG TGCTCCTGAT CCAGCGAGGT 1020
ACCCATTGCC ACTCCCGATC AGGCTAAAGG CTTGCCATTG TTCCCTGCATG GCTAAGTGCC 1080
TGGGTTTGTG CTAATAGAAC TGAACACTGG TCACTGGGTT CCATGGTTCT CTTCCATGAC 1140
CCACGGCTTC TAATAGAGCT ATAACACTCA CCGCATGGCC CAAGATTCCA TICCTTGGTA 1200
TCTGTGAGGC CAAGAACCCCC AGGTCAGAGA ANGTGAGGCT TGCCACCATT TGGGAAGTGG 1260
CCCACTGCCA TTTTGGTAGC GCCCCACCAC CATCTTGGGA CCTGTGGGNG CAAGGATCCC 1320
CCAGTAACA 1329

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

Gln Asn Arg Arg Ala Leu Asp Leu Leu Thr Ala Lys Arg Gly Gly Thr
1 5 10 15
Cys Leu Phe Leu Gly Glu Glu Cys Cys Xaa Tyr Val Asn Gln Ser Gly
20 25 30
Ile Ile Thr Glu Lys Val Lys Glu Ile Xaa Asp Arg Ile Xaa Cys Arg
35 40 45
Ala Glu Asp Leu Gln Asn Thr Ala Pro Trp Gly Leu Leu Ser Gln Trp
50 55 60
Met Pro Trp Thr Leu Pro Phe Leu Gly Pro Leu Ala Ala Ile Ile Phe
65 70 75 80
Leu Leu Leu Phe Gly Pro Cys Ile Phe Asn Phe Leu Val Lys Phe Val
85 90 95
Ser Ser Arg Ile Glu Ala Val Lys Leu Gln Ile Val Leu Gln Met Glu
100 105 110

10

Pro Gln Met Gln Ser Met Thr Lys Ile Tyr Arg Gly Pro Leu Asp Arg
115 120 125
Pro Ala Arg Leu Cys Ser Asp Val Asn Asp Ile Glu Val Thr Pro Pro
130 135 140
Glu Glu Ile Ser Thr Ala Gln Pro Leu Leu His Ser Asn Ser Val Gly
145 150 155 160
Ser Ser

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs
5 (B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

10 GGCATTGATA GCACCCATCA G

21

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs
15 (B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

20 CATGTCACCA GGGTGGAATA G

21

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: base pairs
25 (B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 758 base pairs
(B) TYPE: nucleotide
5 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

GGCATTGATA GCACCCATCA GATGCCAAA TCATTATTTA CTGGACCAGG CCTTTTCAAA 60
ACTATCAAGC AGATAAGGCC CGTGAAGCAT GCCAAAGAAA TAATCCCCTG CCTTATCGCC 120
ATGTTCTTC AGGAGAACAA AGAACAGGCC ATTACCCAGG GGAAGACTGG CAACTAGATT 180
TTACCCACAT GGCCAAATGT CAGGGATTTC AGCATCTACT AGTCTGGGA GATACTTCA 240
CTGGTTGGGT GGAGTCTTCT CCTTGTAGGA CAGAAAGAC CCAAGAGGTA ATAAAGGCAC 300
TAATGAAATA ATTCCCAGAT TTGGACTTCC CCCAGGATTA CAGGGTCACA ATGGCCCCGC 360
TTTCAAGGCT GCAGTAACCC AGGGACTATC CCAGGTGTTA GCCATACAAAT ATCACTTACA 420
CTCTGCCCTGG AGGCCACAAT CCTCCAGAAA ACTCAAGAAA ATGAATGAAA CACTCAAAGA 480
TCTAAAAAAAG CTAACCCAG AAACCCACAT TGCATGACCT GTTCTTTGC CTATAACCTT 540
ACTAAGAACAT CATAACTATC CCCCAAAAAG CAGGACTTAG CCCATACGAG ATGCTATATG 600
GATGGCCTTT CCTAACCAAT GACCTTGTC TTGACTGAGA AATGGCCAAC TTAGTTGCAG 660
ACATCACCTC CTTAGCCAAA TATCAACAAG TTCTTAAAC ATCACAGGGG ACCTGTCCCC 720
GAGAGGAGGG AAAGGAACTA TTCCACCCCTG GTGACATG 758

10 (2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs
(B) TYPE: nucleotide
15 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

CGGACATCCA AAGTGATGGG AAACG

25

20 (2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs
(B) TYPE: nucleotide
25 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

GGACAGGAAA GTAAGACTGA GAAGGC

26

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 26 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

CCTAGAACGT ATTCTGGAGA ATTGGG

26

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 26 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

TGGCTCTCAA TGGTCAAACA TACCCG

26

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 1511 base pairs
(B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

~~CCTAGAACGT ATTCTGGAGA ATTGGGACCA ATGTGACACT CAGACGCTAA GAAACAAACG~~ 60

ATTTATATTCTTCTGCAGTA CGCCCTGGCC ACAATATCCT CTTCAAGGGA GAGAAACCTG 120
GCTTCCTGAG CGAAAGTATAA ATTATAACAT CATCTTACAG CTACACCTCT TCTGTAGAAA 180
GGAGGGCAAA TCGAGTGAAG TGCCATATGT GCAAAATTTG TTTTCATTAA GAGACAACTC 240
ACAATTATGT AAAAAGTGTG GTTATGCC TACAGGAAGC CCTCAGAGTC CACCTCCCTA 300
CCCCAGCGTC CCCTCCCCGA CTCCCTCCCTC AACTAATAAG GACCCCCCTT TAACCCAAAC 360
GGTCCAAAAG GAGATAGACA AACGGCTAAA CAATGAACCA AAGAGTGCCA ATATTCCCCG 420
ATTATGCCCTC TCAGACTTAA AGCAAATTAA AATAGACCTA GGTAATTCTC CAGATAACCC 540
TGACGGCTAT ATTGATGTTT TACAAGGGTT AGGACAATCC TTTCATCTGA CATGGACAGA 600
TATAATGTTA CTACTAAATC AGACACTAAC CCCAAATGAG AGAAGTGCCG CTGTAACCTC 660
ACCCCGAGAG TTTGGCGATC TTTGGTATCT CAGTCAGGCC AACAAATAGGA TGACAACAGA 720
GGAAAGAAACA ACTCCCACAG GCCAGCAGGC AGTTCCCAGT GTAGACCCCTC ATTGGGACAC 780
AGAATCAGAA CATGGAGATT GGTGCCACAA ACATTGCTA ACTTGGTGC TAGAAGGACT 840
GAGGAAAAGT AGGAAGAACG CTATGAATTA CTCAATGATG TCCACTATAA CACAGGGAAA 900
GGAAGAAAAT CTTACTGCTT TTCTGGACAG ACTAAGGGAG GCATTGAGGA AGCATAACCTC 960
CCTGTCACCT GACTCTATTG AAGCCCAACT AATCTAAAG GATAAGTTA TCACTCAGTC 1020
ACCTGCCAGAC ATTAGAAAAA ACTTCAAAAG TCTGCCCTAG GCCCGGAGCA GAACCTAGAA 1080
ACCCATTTA ACTTGGCATC CTCAGTTTT TATAATAGAG ATCAGGAGGA GCAGGGAAA 1140
CGGGACAAAC GGGATAAAAAA AAAAGGGGG GGTCCACTAC TTAGTCATG GCCCTCAGGC 1200
AAGCAGACTT TGGAGGCTCT GCAAAAGGGA AAAGCTGGC AAATCAAATG CCTAATAGGG 1260
CTGGCTTCCA GTGGGTCTA CAAGGACACT TTAAAAAAGA TTATCCAAGT AGAAAATAAGC 1320
CCCCCCTTG TCCATGGCCC TTACGTCAAG GGAATCCTTG GAAGGGCCAC TGCCCCAGGG 1380
GATGAAGATA CTCTGAGTCA GAAGCCATTA ACCAGATGAT CCAGCAGCAG GACTGAGGGT 1440
GCCCGGGGCG AGGCCAGCC CATGCCATCA CCCTCACAGA GCCCCGGGTA TGTTTGACCA 1500
TTGAGAGCCA A 1511

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Leu Glu Arg Ile Leu Glu Asn Trp Asp Gln Cys Asp Thr Gln Thr Leu
10 1 5 10 15

Arg Lys Lys Arg Phe Ile Phe Phe Cys Ser Thr Ala Trp Pro Gln Tyr
20 25 30

Pro Leu Gln Gln Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn Tyr
35 40 45

Asn Ile Ile Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys Trp
50 55 60

Ser Glu Val Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn Ser
65 70 75 80

Gln Leu Cys Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln Ser
85 90 95

Pro Pro Pro Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr Asn
100 105 110

Lys Asp Pro Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys Gly
115 120 125

Val Asn Asn Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro Leu
130 135 140

Gln Ala Val Arg Gly Gly Glu Phe Gly Pro Ala Arg Val Pro Val Pro
145 150 155 160

Phe Ser Leu Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys Phe
165 170 175

Ser Asp Asn Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly Gln
180 185 190

Ser Phe Asp Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln Thr
195 200 205

Leu Thr Pro Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu Phe
210 215 220

Gly Asp Leu Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr Glu
225 230 235 240

Glu Arg Thr Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp Pro
245 250 255

His Trp Asp Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His Leu
260 265 270

Leu Thr Cys Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro Met
275 280 285

Asn Tyr Ser Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn Leu
290 295 300

1 5 10 15
Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
20 25 30
Ile Leu Glu Arg Ile Leu Glu Asn Trp Asp Gln Cys Asp Thr Gln Thr
35 40 45
Leu Arg Lys Lys Arg Phe Ile Phe Phe Cys Ser Thr Ala Trp Pro Gln
50 55 60
Tyr Pro Leu Gln Gly Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn
65 70 75 80
Tyr Asn Ile Ile Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys
85 90 95
Trp Ser Glu Val Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn
100 105 110
Ser Gln Leu Cys Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln
115 120 125
Ser Pro Pro Pro Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr
130 135 140
Asn Lys Asp Pro Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys
145 150 155 160
Gly Val Asn Asn Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro
165 170 175
Leu Gln Ala Val Arg Gly Glu Phe Gly Pro Ala Arg Val Pro Val
180 185 190
Pro Phe Ser Leu Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys
195 200 205
Phe Ser Asp Asn Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly
210 215 220
Gln Ser Phe Asp Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln
225 230 235 240
Thr Leu Thr Pro Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu
245 250 255
Phe Gly Asp Leu Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr
260 265 270
Glu Glu Arg Thr Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp
275 280 285
Pro His Trp Asp Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His

290

295

300

Leu Leu Thr Cys Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro
305 310 315 320
Met Asn Tyr Ser Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn
325 330 335
Leu Thr Ala Phe Leu Asp Arg Leu Arg Glu Ala Leu Arg Lys His Thr
340 345 350
Ser Leu Ser Pro Asp Ser Ile Glu Gly Gln Leu Ile Leu Lys Asp Lys
355 360 365
Phe Ile Thr Gln Ser Ala Ala Asp Ile Arg Lys Asn Phe Lys Ser Leu
370 375 380
Pro Lys Leu Ala Ala Ala Leu Glu His His His His His His
385 390 395

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 378 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Leu Glu Arg
1 5 10 15
Ile Leu Glu Asn Trp Asp Gln Cys Asp Thr Gln Thr Leu Arg Lys Lys
20 25 30
Arg Phe Ile Phe Phe Cys Ser Thr Ala Trp Pro Gln Tyr Pro Leu Gln
35 40 45
Gly Arg Glu Thr Trp Leu Pro Glu Gly Ser Ile Asn Tyr Asn Ile Ile
50 55 60
Leu Gln Leu Asp Leu Phe Cys Arg Lys Glu Gly Lys Trp Ser Glu Val
65 70 75 80
Pro Tyr Val Gln Thr Phe Phe Ser Leu Arg Asp Asn Ser Gln Leu Cys
85 90 95
Lys Lys Cys Gly Leu Cys Pro Thr Gly Ser Pro Gln Ser Pro Pro Pro
100 105 110

10

Tyr Pro Ser Val Pro Ser Pro Thr Pro Ser Ser Thr Asn Lys Asp Pro
115 120 125
Pro Leu Thr Gln Thr Val Gln Lys Glu Ile Asp Lys Gly Val Asn Asn
130 135 140
Glu Pro Lys Ser Ala Asn Ile Pro Arg Leu Cys Pro Leu Gln Ala Val
145 150 155 160
Arg Gly Gly Glu Phe Gly Pro Ala Arg Val Pro Val Pro Phe Ser Leu
165 170 175
Ser Asp Leu Lys Gln Ile Lys Ile Asp Leu Gly Lys Phe Ser Asp Asn
180 185 190
Pro Asp Gly Tyr Ile Asp Val Leu Gln Gly Leu Gly Gln Ser Phe Asp
195 200 205
Leu Thr Trp Arg Asp Ile Met Leu Leu Leu Asn Gln Thr Leu Thr Pro
210 215 220
Asn Glu Arg Ser Ala Ala Val Thr Ala Ala Arg Glu Phe Gly Asp Leu
225 230 235 240
Trp Tyr Leu Ser Gln Ala Asn Asn Arg Met Thr Thr Glu Glu Arg Thr
245 250 255
Thr Pro Thr Gly Gln Gln Ala Val Pro Ser Val Asp Pro His Trp Asp
260 265 270
Thr Glu Ser Glu His Gly Asp Trp Cys His Lys His Leu Leu Thr Cys
275 280 285
Val Leu Glu Gly Leu Arg Lys Thr Arg Lys Lys Pro Met Asn Tyr Ser
290 295 300
Met Met Ser Thr Ile Thr Gln Gly Lys Glu Glu Asn Leu Thr Ala Phe
305 310 315 320
Leu Asp Arg Leu Arg Glu Ala Leu Arg Lys His Thr Ser Leu Ser Pro
325 330 335
Asp Ser Ile Glu Gly Gln Leu Ile Leu Lys Asp Lys Phe Ile Thr Gln
340 345 350
Ser Ala Ala Asp Ile Arg Lys Asn Phe Lys Ser Leu Pro Lys Leu Ala
355 360 365
Ala Ala Leu Glu His His His His His His
370 375

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

CTTGGAGGGT GCATAACCAAG GGAAT

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(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleotide

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

TGTCCGCTGT GCTCCTGATC

20

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(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleotide

20 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

CTATGTCCTT TTGGACTGTT TGGGT

25

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(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 764 base pairs

(B) TYPE: nucleotide

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TGTCCGCTGT GCTCCTGATC CAGCACAGGC GCCCATGCC TCTCCAATT GGGCTAAAGG 60
CTTGGCCATTG TTCCCTGCACA GCTAAGTCGC TGGGTTCATC CTAATCGAGC TGAACACTAG 120
TCACTGGGTT CCACGGTTCT CTTCCATGAC CCATGGCTTC TAATAGAGCT ATAACACTCA 180
CTGCATGGTC CAAGATTCCA TTCCCTGGAA TCCGTGAGAC CAAGAACCCC AGGTCAGAGA 240
ACACAAGGCT TGCCACCAGT TTGGAAGCAG CCCACCCACCA TTTTGGAAAGC AGCCCGCCAC 300
TATCTTGGGA GCTCTGGGAG CAAGGACCCC AGGTAAACAAT TTGGTGACCA CGAAGGGACC 360
TGAATCCGCA ACCATGAAGG GATCTCCAAA GCAATTGGAA ATGTTCCCTCC CAAGGCAAAA 420
ATGCCCCCTAA GATGTATTCT GGAGAATTGG GACCAATTG ACCCTCAGAC AGTAAGAAAA 480
AAATGACTTA TATTCTTCTG CAGTACCGCC CTGGCCACGA TATCCTCTTC AAGGGGGAGA 540
AACCTGGCT CCTGAGGGAA CTATAAATTA TAACACCACAC TTACAGCTAC ACCTGTTTTC 600
TAGAAAAGGA GGCIAATGGA GTGAAGTGCC ATATTACAA ACTTTCTTTT CATTAAAAGA 660
CAACTCCCAA TTATGTTAAC AGTGTGATT GTGTTCCCTAC ACGGAAGCCC TCAGATTCTA 720
CTCCCCACCC CGGGCATCTC CCCTGAATCC CTCCCCAACT TATT 784

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 800 base pairs
5 (B) TYPE: nucleotide
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

TGTCCGCTGT GCTCCTGATC CAGCACAGGC GCCCATGCC TCTCCAATT GGGCTAAAGG 60
CTTGGCCATTG TTCCCTGCACA GCTAAGTCGC TGGGTTCATC CTAATCGAGC TGAACACTAG 120
TCACTGGGTT CCACGGTTCT CTTCCATGAC CCATGGCTTC TAATAGAGCT ATAACACTCA 180
CTGCATGGTC CAAGATTCCA TTCCCTGGAA TCCGTGAGAC CAAGAACCCC AGGTCAGAGA 240
ACACAAGGCT TGCCACCAGT TTGGAAGCAG CCCACCCACCA TTTTGGAAAGC GGGGGGGCAC 300
TATCTTGGGA GCTCTGGGAG CAAGGACCCC CAGGTAACAA TTTGGTGACCA CGAAGGGACC 360
CTGAATCCGCA ACCATGAAG GGTCTCCAAA AGCAATTGGAA ATGTTCCCTC CAAGGCAAAA 420
AAATCCCCCTA AGATGTATTG TGGAGAATTG GGACCAATCT GACCCCTCAGA CAGTAAGAAA 480
AAAAATGACT TATATTCTTC TGCAGTACCG CCTGGCCACG GATATCCTCT TCAAGGGGGAGA 540
GAAACCTGGC CTCCCTGAGGG AAGTATAAAT TATAACACCA TCTTACAGCT AGACCTGTTT 600
TGTAGAAAAG GAGGCIAATG GAGTGAAGTG CCATATTTAC AAACTTCTT TTCATTAAAAA 660
GACAACCTCGC AATTATGTAA ACAGTGTGAT TGTGTCCTA CAGGAAGCCC TCAGATCTAC 720
CTCCCCACCC CGGGCATCTC CCCTGAATCC CTCCCCAACTAA TAAGGACCCCA CTTCAGCCCCA 780
10 AACAGTCCAA AAGGACATAG 800